

Remarks

Upon entry of the foregoing amendment, claims 1-46 are pending in the application, with claims 1, 14, 32, 34, 38, 40, 41 and 44 being the independent claims. Applicants have amended claim 31 to make it dependent on claim 14. Support for the amendment to claim 31 may be found, *inter alia*, in Example 39. These changes are believed to introduce no new matter, and their entry is respectfully requested.

Election

The Examiner requested an election of an invention directed to one of the following of Groups I-DXCI. Groups CCLXXXI-CCCVI, corresponding to claims 14-15 and 19-30 and newly amended claim 31, are drawn to a method of identifying potentially therapeutic anticancer compounds comprising contacting one Transferrin Receptor Related Apoptosis Inducing Protein with test compounds, wherein compounds that bind one Transferrin Receptor Related Apoptosis Inducing Protein are potentially therapeutic anticancer compound. The Examiner has requested an election of one Transferrin Receptor Related Apoptosis Inducing Protein, corresponding to one of SEQ ID NOS:1-26.

Applicants hereby provisionally elect to prosecute the invention of Group CCLXXXI, represented by claims 14-15 and 19-30 and newly amended claim 31. Applicants further elect SEQ ID NO:1 and the species 1-(3-methyl-2-butenyl)-3,3-dimethyl-1,3,3a,4,5,12a-hexahydro-7,13-dioxo-1,5-methano-furo[3,4-d]xanthene of

claim 31. This election is made without prejudice to or disclaimer of the other claims or inventions disclosed.

This election is made with traverse.

Applicants respectfully request rejoinder of groups CCLXXXI-CCCVI. While the Examiner has required election of one of SEQ ID NOS:1-26 for prosecution, Applicants respectfully point out to the Examiner that SEQ ID NOS:1-26 are related sequences. Applicants attach herewith sequence alignments of SEQ ID NO:1 and SEQ ID NOS:2-26 generated by BLAST (Basic Local Alignment Search Tool). As seen from the alignments, SEQ ID NOS:1, 2, 3 and 8 are identical sequences. Further, there is only one amino acid difference between SEQ ID NO:1 and SEQ ID NOS:4, 5, 6, 9 and 10. Further, SEQ ID NOS:11-21 are fragments of 639 or 640 amino acids in length and have one or three amino acid differences (greater than 99% identical) compared with the corresponding fragments in SEQ ID NO:1. Therefore, at a minimum, Applicants request that the Examiner rejoin Groups CCLXXXII-CCLXXXVI and CCLXXXVIII-CCXC (corresponding to SEQ ID NOS:2-6 and SEQ ID NOS:8-10) with Group CCLXXXI, because the sequences are identical or differ by only one amino acid and would therefore involve the same search. Likewise, Groups CCXCI-CCCI (corresponding to SEQ ID NOS:11-21) should be rejoined with Group CCLXXXI on the same basis. SEQ ID NOS:7 and 22-26 are smaller fragments of 15-63 amino acids and share from 81-100% identity with the corresponding fragments of SEQ ID NO:1. Therefore, a search of SEQ ID NO:1 would necessarily be coextensive with a search for these sequences as well and

Applicants respectfully request rejoinder of Groups CCLXXXVII and CCCII-CCCVI with Group CCLXXXI.

Reconsideration and withdrawal of the Restriction Requirement, and consideration and allowance of all pending claims, are respectfully requested. It is not believed that extensions of time are required, beyond those that may otherwise be provided for in accompanying documents. However, if additional extensions of time are necessary to prevent abandonment of this application, then such extensions of time are hereby petitioned under 37 C.F.R. § 1.136(a), and any fees required therefor are hereby authorized to be charged to our Deposit Account No. 19-0036.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.



Robert W. Esmond
Attorney for Applicants
Registration No. 32,893

Date: Nov. 20, 2006

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Washington, D.C. 20005-3934
(202) 371-2600

599905_1.DOC



Blast 2 Sequences results

PubMed

Entrez

BLAST

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Taxonomy

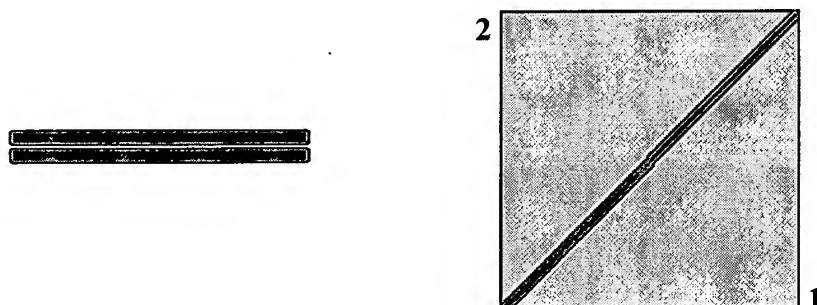
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|6164848|gb|AAF04564.1|AF187320_1transferrin receptor [Homo sapiens]
 >gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr)
 (CD71 antigen) (T9) (p90) >gi|12654697|gb|AAH01188.1| TFRC protein [Homo sapiens]
 >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1531 bits (3964), Expect = 0.0

Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)

SEQUENCE:

1

2

Query	1	MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	60
		MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	
Sbjct	1	MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	60
Query	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
		RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	
Sbjct	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
Query	121	RLYWDDLKRKLSEKLDSTDFGTG I KLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180
		RLYWDDLKRKLSEKLDSTDFGTG I KLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	
Sbjct	121	RLYWDDLKRKLSEKLDSTDFGTG I KLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180

```

Query 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
Sbjct 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240

Query 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Sbjct 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300

Query 301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360
Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360

Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG 420
Sbjct 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG 420

Query 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480
Sbjct 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480

Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Sbjct 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540

Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
Sbjct 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600

Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIEMGLSLQWLYSARGDFFRATSRLTTDF 660
Sbjct 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIEMGLSLQWLYSARGDFFRATSRLTTDF 660

Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRHFWGSGSHTLPALLENLKLRLK 720
Sbjct 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRHFWGSGSHTLPALLENLKLRLK 720

Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
Sbjct 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760

```

CPU time: 0.04 user secs. 0.02 sys. secs 0.06 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

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Number of Sequences: 1

Number of Hits to DB: 4468

Number of extensions: 2537

Number of successful extensions: 1

Number of sequences better than 10.0: 1

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Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,435,209,301
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,435,209,158
Effective search space: 885524050486
Effective search space used: 885524050486
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
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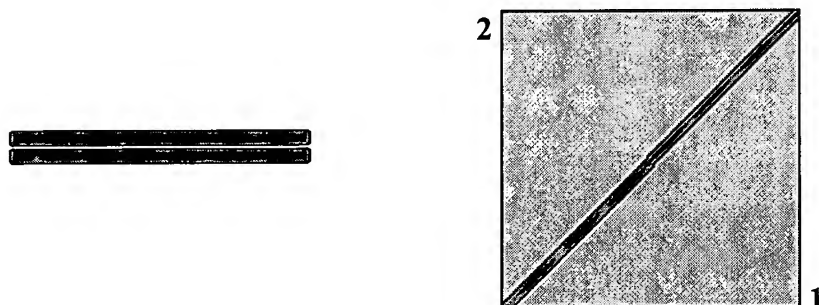
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 >gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90) >gi|6164848|gb|AAF04564.1|AF187320_1 transferrin receptor [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)



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Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)

SEQUENCE

1	Query	1	MMDQARSFAFSNLFGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
			MMDQARSFAFSNLFGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
3	Sbjct	1	MMDQARSFAFSNLFGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
	Query	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
			RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
	Sbjct	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
	Query	121	RLYWDDLKRKLSEKLDSTDFGTIKLLN ENSYVPREAGSQKDENLALYVENQFREFKLSK	180
			RLYWDDLKRKLSEKLDSTDFGTIKLLN ENSYVPREAGSQKDENLALYVENQFREFKLSK	180
	Sbjct	121	RLYWDDLKRKLSEKLDSTDFGTIKLLN ENSYVPREAGSQKDENLALYVENQFREFKLSK	180

```

Query 181 VWRDQHFKIQVKDSAQNSV IVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
Sbjct 181 VWRDQHFKIQVKDSAQNSV IVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240

Query 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Sbjct 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300

Query 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360
Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360

Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSG 420
Sbjct 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSG 420

Query 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT 480
Sbjct 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT 480

Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Sbjct 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540

Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAA EVAGQFVIK 600
Sbjct 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAA EVAGQFVIK 600

Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
Sbjct 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660

Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RK 720
Sbjct 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RK 720

Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
Sbjct 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

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Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
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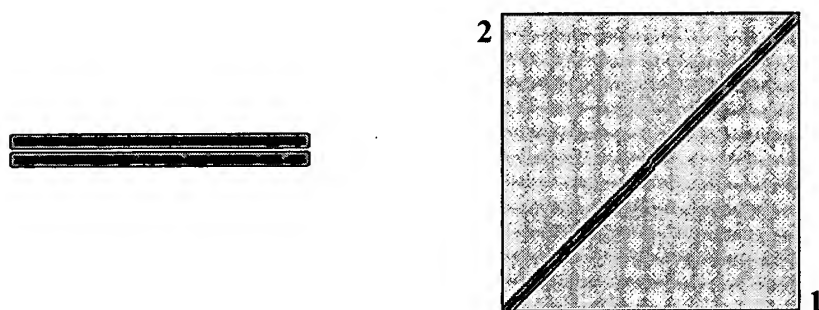
Structure

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Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: gi|4507457|ref|NP_003225.1|transferrin receptor [Homo sapiens]
>gi|37433|emb|CAA25527.1| unnamed protein product [Homo sapiens] >gi|339516|gb|AAA61153.1|
transferrin receptor >gi|224192|prf|1011297A transferrin receptor
Length = 760 (1 .. 760)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1529 bits (3958), Expect = 0.0

Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

Station 1

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			MMDQARSFAFSNLFSGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	60
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	Query	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
			RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
	Sbjct	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
	Query	121	RLYWDDLKRKLSEKLDSTDF TGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180
			RLYWDDLKRKLSEKLDSTDF TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180
	Sbjct	121	RLYWDDLKRKLSEKLDSTDF TSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180
	Query	181	VWRDQHFKVIQVKDS AQNSVIIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTK	240

```

Sbjct 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
Query 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
          KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Query 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 360
          AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 360
Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG 420
          STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG
Sbjct 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG 420
Query 421 VGTALLKLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480
          VGTALLKLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT
Sbjct 421 VGTALLKLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480
Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
          YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
          AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIEMGLSLQWLYSARGDFFRATSRLTTDF 660
          LTHDVELNLDYERYNSQLLSFVRDLNQYRADIEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIEMGLSLQWLYSARGDFFRATSRLTTDF 660
Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK 720
          GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK
Sbjct 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK 720
Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760

```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

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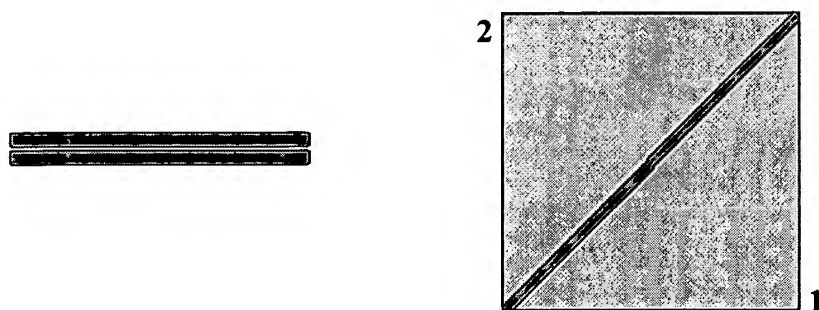
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Sequence 2: gi|37433|emb|CAA25527.1|unnamed protein product [Homo sapiens]
 >gi|4507457|ref|NP_003225.1| transferrin receptor [Homo sapiens] >gi|339516|gb|AAA61153.1|
 transferrin receptor >gi|224192|prf||1011297A transferrin receptor
 Length = 760 (1 .. 760)



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 1 Query 1 MMDQARSFNSLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK 60
 5 Sbjct 1 MMDQARSFNSLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK 60
 Query 61 RCGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDF PAAR 120
 Sbjct 61 RCGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDF PAAR 120
 Query 121 RLYWDDLKRKLSEKLDSTDF TGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180
 Sbjct 121 RLYWDDLKRKLSEKLDSTDF TSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180
 Query 181 VWRDQHFVKIQVKDSAQNSVI IVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTK 240

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Sbjct 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
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          KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Query 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360
          AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD
Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360
Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG 420
          STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG
Sbjct 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSG 420
Query 421 VGTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT 480
          VGTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT
Sbjct 421 VGTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT 480
Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
          YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
          AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
          LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK 720
          GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK
Sbjct 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK 720
Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 4451

Number of extensions: 2525

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

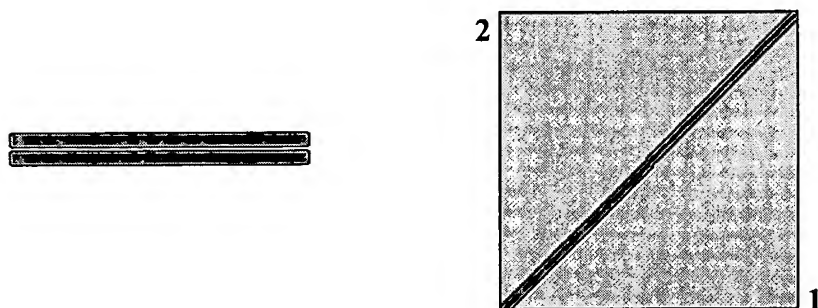
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|339516|gb|AAA61153.1|transferrin receptor >gi|4507457|ref|NP_003225.1| transferrin receptor [Homo sapiens] >gi|37433|emb|CAA25527.1| unnamed protein product [Homo sapiens] >gi|224192|prf|1011297A transferrin receptor
 Length = 760 (1 .. 760)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1529 bits (3958), Expect = 0.0

Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

562DNO
 1
 6

Query	1	MMDQARSFNSNLFGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	60
		MMDQARSFNSNLFGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	60
Sbjct	1	MMDQARSFNSNLFGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVTKPK	60
Query	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
		RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
Sbjct	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
Query	121	RLYWDDLKRKLSEKLDSTDFGTIKLLNENS YVPREAGSQKDENLALYVENQFREFKLSK	180
		RLYWDDLKRKLSEKLDSTDFGTIKLLNENS YVPREAGSQKDENLALYVENQFREFKLSK	180
Sbjct	121	RLYWDDLKRKLSEKLDSTDFGTIKLLNENS YVPREAGSQKDENLALYVENQFREFKLSK	180
Query	181	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTK	240


```

Sbjct 181 VWRDQHFKVIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
Query 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH
Sbjct 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Query 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 360
AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD
Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD 360
Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG 420
STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG
Sbjct 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKSG 420
Query 421 VGTALLKLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480
VGTALLKLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT
Sbjct 421 VGTALLKLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480
Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK
Sbjct 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLRLK 720
GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLRLK
Sbjct 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLRLK 720
Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760

```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 4451

Number of extensions: 2525

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

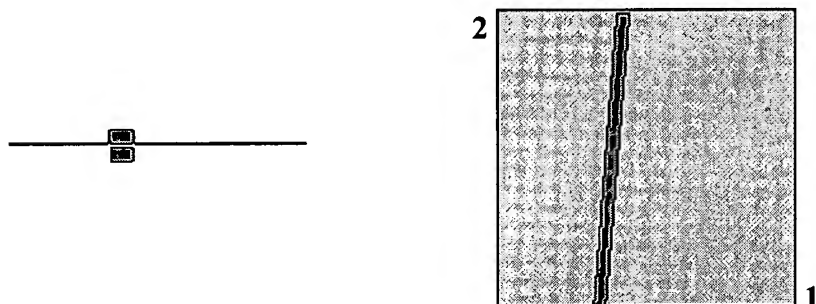
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix **BLOSUM62** ☐ gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option **Standard** ☐
 Masking character option **X for protein, n for nucleotide** ☐ Masking color option **Black** ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|1336700|gb|AAB35972.1|transferrin receptor; TfR [Cavia] >gi|2144140|pir||S68317
 transferrin receptor - guinea pig (fragment)
 Length = 63 (1 .. 63)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 118 bits (295), Expect = 2e-24
 Identities = 54/63 (85%), Positives = 57/63 (90%), Gaps = 0/63 (0%)

SEQUENCE
 1
 7
 Query 261 KITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSF FGHHLGTGDPYTPGFPSFNHTQ 320
 KITFAEKVANAESLNA+GVLIY+D TKFPI A+L FGH HLGTGDPYTPGFPSFNHTQ
 Sbjct 1 KITFAEKVANAESLNALGVLIYLDWTKFPIPKADLPVFGHVHLGTGDPYTPGFPSFNHTQ 60
 Query 321 FPP 323
 FPP
 Sbjct 61 FPP 63

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H

0.318 0.135 0.399

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 413

Number of extensions: 242

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.7 bits)

S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

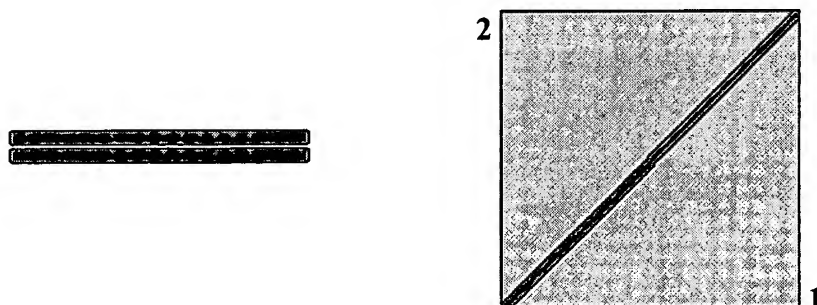
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]

Length = 760 (1 .. 760)

Sequence 2: gi|108935939|sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 antigen) (T9) (p90) >gi|6164848|gb|AAF04564.1|AF187320_1 transferrin receptor [Homo sapiens] >gi|12654697|gb|AAH01188.1| TFRC protein [Homo sapiens] >gi|94717625|gb|ABF47088.1| transferrin receptor (p90, CD71) [Homo sapiens]

Length = 760 (1 .. 760)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1531 bits (3964), Expect = 0.0

Identities = 760/760 (100%), Positives = 760/760 (100%), Gaps = 0/760 (0%)

8 QID NO

1	Query	1	MMDQARSFNSNLFSGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
			MMDQARSFNSNLFSGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	
8	Sbjct	1	MMDQARSFNSNLFSGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
	Query	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
			RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	
	Sbjct	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
	Query	121	RLYWDDLKRKLSEKLDSTDFGTIKLLN ENSYVPREAGSQKDENLALYVENQFREFKLSK	180
			RLYWDDLKRKLSEKLDSTDFGTIKLLN ENSYVPREAGSQKDENLALYVENQFREFKLSK	
	Sbjct	121	RLYWDDLKRKLSEKLDSTDFGTIKLLN ENSYVPREAGSQKDENLALYVENQFREFKLSK	180

```

Query 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
Sbjct 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240

Query 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Sbjct 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300

Query 301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360
Sbjct 301 AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTIISRAAAEKLFGNMEGDCPSDWKTD 360

Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG 420
Sbjct 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG 420

Query 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSVGATEWLEGYLSLHLKAFT 480
Sbjct 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSVGATEWLEGYLSLHLKAFT 480

Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Sbjct 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540

Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
Sbjct 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600

Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
Sbjct 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660

Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLRLK 720
Sbjct 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLRLK 720

Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
Sbjct 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760

```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 4468

Number of extensions: 2537

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

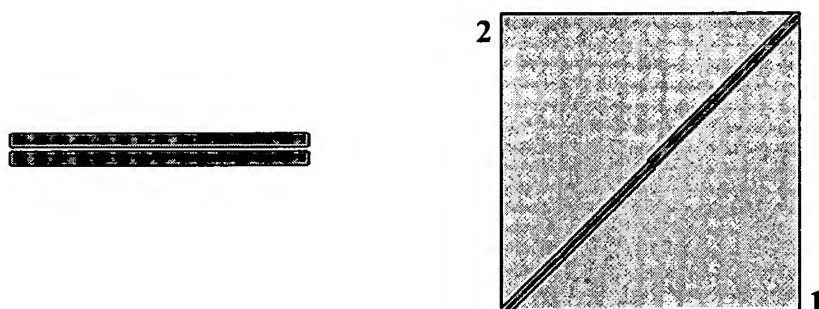
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
 Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: lcl|1_seq_1
 Length = 2249 (1 .. 2249)

Sequence 2: lcl|2_seq_2
 Length = 2249 (1 .. 2249)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 3152 bits (8171), Expect = 0.0

Identities = 2246/2249 (99%), Positives = 2246/2249 (99%), Gaps = 0/2249 (0%)

Seq ID NO

1	Query	1	METMETASPGLNALAARGSERALAPHESERASNLEUPHEXXXXXXXXXPRLEUSERTYRT	60
			METMETASPGLNALAARGSERALAPHESERASNLEUPHEGLYGLYGLUPRLEUSERTYRT	
9	Sbjct	1	METMETASPGLNALAARGSERALAPHESERASNLEUPHEGLYGLYGLUPRLEUSERTYRT	60
	Query	61	HRARGPHERSERLEUALAARGGLNVALASPGLYASPNSEHISVALGLUMETXXXXXXX	120
			HRARGPHERSERLEUALAARGGLNVALASPGLYASPNSEHISVALGLUMETLYSLEUA	
	Sbjct	61	HRARGPHERSERLEUALAARGGLNVALASPGLYASPNSEHISVALGLUMETLYSLEUA	120
	Query	121	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTHRLYSALAASNVALTHRLYSPRLYSAR	180
			LAVALASPLUGLUGLUASNALAASPASNANTHRLYSALAASNVALTHRLYSPRLYSAR	
	Sbjct	121	LAVALASPLUGLUGLUASNALAASPASNANTHRLYSALAASNVALTHRLYSPRLYSAR	180
	Query	181	GCYSSERGLYSERILECYSTYRGLYTHRXXXXXXXXXXXXXXXXXXXXXXXXXXXXYYPH	240
			GCYSSERGLYSERILECYSTYRGLYTHRILEALAVALILEVALPHEPHELEUILEGLYPH	
	Sbjct	181	GCYSSERGLYSERILECYSTYRGLYTHRILEALAVALILEVALPHEPHELEUILEGLYPH	240

Query	241	EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSXXXXXXXXXX	300
Sbjct	241	EMETILEGLYTYRLEUGLYTYRCYSLYSGLYVALGLUPRLYSTHRGLUCYSGLUARGLEU	300
Query	301	XXXXXYTHRGLUSEXXXXXXXXXXXXXXXXXXXXXUASPPHEPXXXXXXXXXXXXXEU	360
Sbjct	301	ALAGLYTHRGLUSERPRVALARGGLUGLUPRGLYGLUASPPHEPRALAALAARGARGLEU	360
Query	361	TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHRGLY	420
Sbjct	361	TYRTRPASPASPLEULYSARGLYSLEUSERGLULYSLEUASPSERTHRASPPHETHR	420
Query	421	THRIXXXXXXXXXXASNGLUASNSERTYXXXXXXXXXXXXXXXXXXYSERGLNLYSASPG	480
Sbjct	421	THRIEULYSLEULEUASNGLUASNSERTYRVALPRARGGLUALAGLYSERGLNLYSASPG	480
Query	481	LUASNXXXXXXXXTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA	540
Sbjct	481	LUASNLEUALALEUTYRVALGLUASNGLNPHEARGGLUPHELYSLEUSERLYSVALTRPA	540
Query	541	RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSPERALAGLNASNSERXXXXXXXXXX	600
Sbjct	541	RGASPGLNHISPHEVALLYSILEGLNVALLYSASPSPERALAGLNASNSERVALILEILEV	600
Query	601	XXXSPLYASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE	660
Sbjct	601	ALASPLYASNGLYARGLEUVALTYRLEUVALGLUASNPRGLYGLYTYRVALALATYRSE	660
Query	661	RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHGLYTHRLYSLYSASPPH	720
Sbjct	661	RLYSALAALATHRVALTHRGLYLYSLEUVALHISALAASNPHGLYTHRLYSLYSASPPH	720
Query	721	EGLUASPLEUTYRTHRPRVALASNGLYSERXXXXXXXXXXXXXXXXXXXXXSIETHR	780
Sbjct	721	EGLUASPLEUTYRTHRPRVALASNGLYSERILEVALILEVALARGALAGLYLYSILETHR	780
Query	781	PHEXXXXXXXXXXXXXXXXXXXXXXXXXERLEUASNALAILEGLYVALLEUILETYRMET	840
Sbjct	781	PHEALAGLULYSVALALAASNALAGLUSERLEUASNALAILEGLYVALLEUILETYRMET	840
Query	841	ASPGLNTHRLYSPHEPRILEVXXXXXXXXXXXXXEUERPHEPHEGLYHISALAHISLEUG	900
Sbjct	841	ASPGLNTHRLYSPHEPRILEVALASNALAGLULEUSERPHEPHEGLYHISALAHISLEUG	900
Query	901	LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTRGLNPHEPRPRSERARG	960
Sbjct	901	LYTHRGLYASPPRTYRTHRPRGLYPHEPRSERPHEASNHISTRGLNPHEPRPRSERARG	960
Query	961	XXXXXXXXLYLEUPRASNILEPRVALGLNTHRISEXXXXXXXXXXXXXXXXXXYSLEUPH	1020
Sbjct	961	SERSERGLYLEUPRASNILEPRVALGLNTHRISEERARGALAALAALAGLULYSLEUPH	1020
Query	1021	EGLYASNMETGLUGLYASPCYSPRSEASPTRPLYSTHRASPSERTHRCYSARGMETVAL	1080
Sbjct	1021	EGLYASNMETGLUGLYASPCYSPRSEASPTRPLYSTHRASPSERTHRCYSARGMETVAL	1080
Query	1081	THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVALXXXXXXXXXXXXXXXXXX	1140
Sbjct	1081	THRSERGLUSERLYSASNVALLYSLEUTHRVALSERASNVALLEULYSGLUILELYSILE	1140

Query	1141	XXUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRXXXXXXXXXXXXX	1200
Sbjct	1141	LEUASNILEPHEGLYVALILELYSGLYPHEVALGLUPRASPHISTYRVALVALVALGLYA	1200
Query	1201	XXXXXXXXXXSPALATRPGLYPRGXXXXXXXXXXSSERGLYVALGLYTHRXXXXXXXXXX	1260
Sbjct	1201	LAGLNARGASPALATRPGLYPRGLYALAALALYSSERGLYVALGLYTHRALLALEULE	1260
Query	1261	XXXXXXXXXXNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER	1320
Sbjct	1261	ULYSLEUALAGLNMETPHESERASPMETVALLEULYSASPGLYPHEGLNPRSERARGSER	1320
Query	1321	ILEILEPHEALASERTRPSERLAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU	1380
Sbjct	1321	ILEILEPHEALASERTRPSERLAGLYASPPHEGLYSERVALGLYALATHRGLUTRPLEU	1380
Query	1381	GLUGLYTYXXXXXXXXXXXXXXXXXXXXXYSALAPHETHRTYRILEASNLEUASPLYSALA	1440
Sbjct	1381	GLUGLYTYRLEUSERSERLEUHIISLEULYSALAPHETHRTYRILEASNLEUASPLYSALA	1440
Query	1441	VALLEUGLYTHRSEASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL	1500
Sbjct	1441	VALLEUGLYTHRSEASNPHELYSVALSERALASERPRLEULEUTYRTHRLEUILEGLUL	1500
Query	1501	YSTRMETGLNASNVALLYSHISPRVALTHRGYGLNPHELEUTYRGLNASPSEASNTR	1560
Sbjct	1501	YSTRMETGLNASNVALLYSHISPRVALTHRGYGLNPHELEUTYRGLNASPSEASNTR	1560
Query	1561	PALASERLYSVALGLULYSLEUTHRLEXXXXXXXXXXXXXXHEPRPHELEUALATYRSE	1620
Sbjct	1561	PALASERLYSVALGLULYSLEUTHRLEUASPASNALAALAPHEPRPHELEUALATYRSE	1620
Query	1621	GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH	1680
Sbjct	1621	GLYILEPRALAVALSERPHECYSPHECYSGLUASPTHRASPTYRPRTYRLEUGLYTHRTH	1680
Query	1681	RMETASPTHRTYRLYSXXXXXXXXXXXXXUARGILEPRGLULEUASNLYSVXXXXXXXXXX	1740
Sbjct	1681	RMETASPTHRTYRLYSGLULEUILEGLUARGILEPRGLULEUASNLYSVALALAARGALA	1740
Query	1741	XXXXXXXXXXXXXXXXXXXXXNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU	1800
Sbjct	1741	ALAALAGLUVALALAGLYGLNPHEVALILELYSLEUTHRHISASPVALGLULEUASNLEU	1800
Query	1801	ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG	1860
Sbjct	1801	ASPTYRGLUARGTYRASNSERGLNLEULEUSERPHEVALARGASPLEUASNGLNTYRARG	1860
Query	1861	ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSEALAAARGGLYASPPHE	1920
Sbjct	1861	ALAASPILELYSGLUMETGLYLEUSERLEUGLNTRPLEUTYRSEALAAARGGLYASPPHE	1920
Query	1921	PHEARGALATHRSEARGLLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE	1980
Sbjct	1921	PHEARGALATHRSEARGLLEUTHRTHRASPPHEGLYASNALAGLULYSTHRASPARGPHE	1980
Query	1981	VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV	2040
Sbjct	1981	VALMETLYSLYSLEUASNASPARGVALMETARGVALGLUTYRHISPHELEUSERPRTYRV	2040

```

Query   2041  ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHXXXXXXX 2100
          ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHRLEUPRA
Sbjct   2041  ALSERPRLYSGLUSERPRPHEARGHISVALPHETRPGLYSERGLYSERHISTHRLEUPRA 2100

Query   2101  XXXXXXXXGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP 2160
          LALEULEUGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP
Sbjct   2101  LALEULEUGLUASNLEULYSLEUARGLYSGLNASNASNGLYALAPHEASNGLUTHRLEUP 2160

Query   2161  HEARGASNGLNXXXXXXXXXXXXXTHRTRPTHRIRXXXXXXXXXXXXXXXXXXXXXXXXXERG 2220
          HEARGASNGLNLEUALALEUALATHRTRPTHRILEGLNGLYALAALAASNALALEUSERG
Sbjct   2161  HEARGASNGLNLEUALALEUALATHRTRPTHRILEGLNGLYALAALAASNALALEUSERG 2220

Query   2221  LYASPVALTRPASPILEASPASNGLUPHE 2249
          LYASPVALTRPASPILEASPASNGLUPHE
Sbjct   2221  LYASPVALTRPASPILEASPASNGLUPHE 2249

```

CPU time: 0.05 user secs. 0.01 sys. secs 0.06 total secs.

```

Lambda        K            H
         0.314        0.130        0.376

```

Gapped

```

Lambda        K            H
         0.267        0.0410        0.140

```

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 94,211

Number of extensions: 37877

Number of successful extensions: 747

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 2249

Length of database: 1,435,209,301

Length adjustment: 151

Effective length of query: 2098

Effective length of database: 1,435,209,150

Effective search space: 3011068796700

Effective search space used: 3011068796700

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (22.0 bits)

S2: 88 (38.5 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

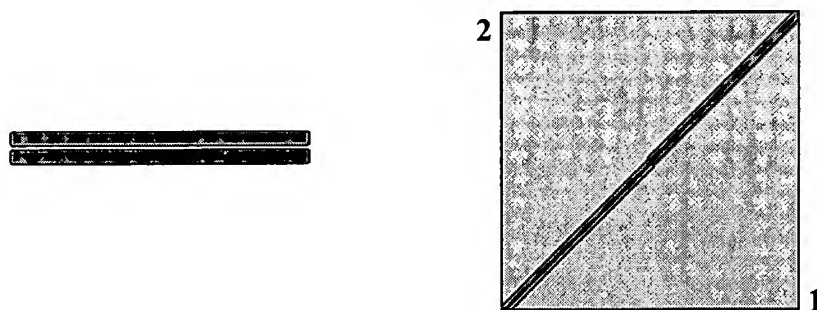
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
 Length = 760 (1 .. 760)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1529 bits (3958), Expect = 0.0

Identities = 759/760 (99%), Positives = 759/760 (99%), Gaps = 0/760 (0%)

SEQUENCE

1	Query	1	MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
			MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	
10	Sbjct	1	MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDN SHVEMKLAVDEEENADNNTKANVT KPK	60
	Query	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
			RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	
	Sbjct	61	RCSGSICYGTIAVIVFFLIGFMIGYLG YCKGVEPKTECERLAGTESPVREEPGEDFPAAR	120
	Query	121	RLYWDDLKRKLSEKLDSTDFGTI KLLNENSYPREAGSQKDNLALYVENQFREFKLSK	180
			RLYWDDLKRKLSEKLDSTDFGTI KLLNENSYPREAGSQKDNLALYVENQFREFKLSK	
	Sbjct	121	RLYWDDLKRKLSEKLDSTDFGTI KLLNENSYPREAGSQKDNLALYVENQFREFKLSK	180
	Query	181	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTK	240
			VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTK	
	Sbjct	181	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTK	240

```

Query   241   KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH   300
Sbjct   241   KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH   300

Query   301   AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD   360
Sbjct   301   AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTD   360

Query   361   STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG   420
Sbjct   361   STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG   420

Query   421   VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT   480
Sbjct   421   VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFT   480

Query   481   YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA   540
Sbjct   481   YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA   540

Query   541   AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK   600
Sbjct   541   AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK   600

Query   601   LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF   660
Sbjct   601   LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF   660

Query   661   GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK   720
Sbjct   661   GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK   720

Query   721   QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   760
Sbjct   721   QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   760

```

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 4451

Number of extensions: 2525

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

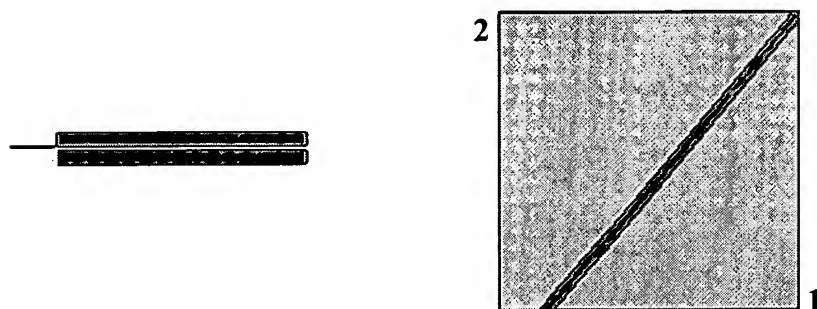
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

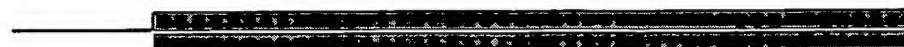
Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 640 (1 .. 640)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1286 bits (3327), Expect = 0.0

Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)

Query 121 RLYWDDLKRKLSEKLDSTDFGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 180
Sbjct 1 RLYWDDLKRKLSEKLDSTDFGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK 60
Query 181 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 240
Sbjct 61 VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK 120
Query 241 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 300
Sbjct 121 KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH 180
Query 301 AHLGTGDPYTPGFPSFNHTQFPSSRSSLNIPVQTISRAAAEKLFNMEGDCPSDWKTD 360
Sbjct 181 AHLGTGDPYTPGFPSFNHTQFPSSRSSLNIPVQTISRAAAEKLFNMEGDCPSDWKTD 240

```

Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG 420
          STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG
Sbjct 241 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG 300

Query 421 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 480
          VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT
Sbjct 301 VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT 360

Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
          YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA
Sbjct 361 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 420

Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAA EVAGQFVIK 600
          AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAA EVAGQFVIK
Sbjct 421 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAA EVAGQFVIK 480

Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
          LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF
Sbjct 481 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 540

Query 661 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK 720
          GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK
Sbjct 541 GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK 600

Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 601 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 640

```

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3743

Number of extensions: 2118

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

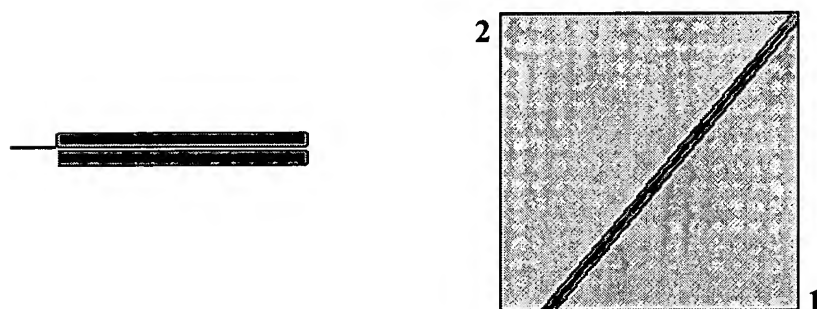
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐Masking character option X for protein, n for nucleotide Masking color option Black ☐☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]

Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2

Length = 640 (1 .. 640)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1286 bits (3327), Expect = 0.0

Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)

SEQUIDNO

(Query	121	RLYWDDLKRKLSEKLDSTDFGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	180
			RLYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	
12	Sbjct	1	RLYWDDLKRKLSEKLDSTDFSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSK	60
	Query	181	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	240
			VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	
	Sbjct	61	VWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	120
	Query	241	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	300
			KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	
	Sbjct	121	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	180
	Query	301	AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFNGMEGDCPSDWKTD	360
			AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFNGMEGDCPSDWKTD	
	Sbjct	181	AHLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFNGMEGDCPSDWKTD	240

```

Query 361 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG 420
Sbjct 241 STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG 300

Query 421 VGTALLLKLAQMFSDMVLKDGFPQRSRIIFASWSAGDFGSGATEWLEGYLSSLHLKAFT 480
Sbjct 301 VGTALLLKLAQMFSDMVLKDGFPQRSRIIFASWSAGDFGSGATEWLEGYLSSLHLKAFT 360

Query 481 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 540
Sbjct 361 YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA 420

Query 541 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 600
Sbjct 421 AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK 480

Query 601 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 660
Sbjct 481 LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF 540

Query 661 GNAEKTDRFVMKKLNDVRMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK 720
Sbjct 541 GNAEKTDRFVMKKLNDVRMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLK 600

Query 721 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
Sbjct 601 QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 640

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3743

Number of extensions: 2118

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

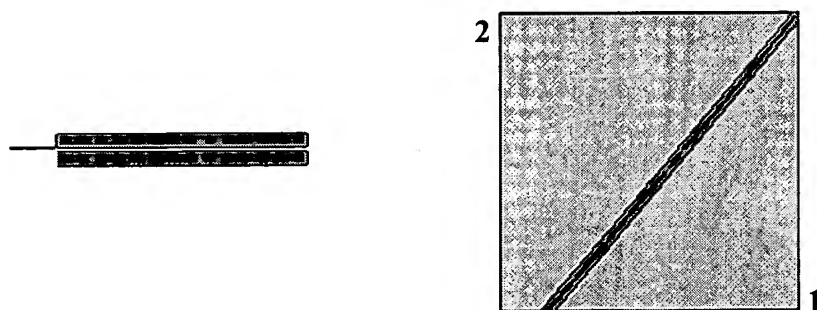
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
Length = 640 (1 .. 640)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1286 bits (3327), Expect = 0.0

Identities = 639/640 (99%), Positives = 639/640 (99%), Gaps = 0/640 (0%)

13

Query	121	RLYWDDLKRKLSEKLDSTDFGTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSK	180
Sbjct	1	RLYWDDLKRKLSEKLDSTDFTTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSK	60
Query	181	VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	240
Sbjct	61	VWRDQHFVKIQVKDSAQNSVIIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTK	120
Query	241	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	300
Sbjct	121	KDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGH	180
Query	301	AHLGTGDPYTPGFPSFNHTQFPSSRSSLNPVQTIISRAAAEKLFGNMEGDCPSDWKTD	360
Sbjct	181	AHLGTGDPYTPGFPSFNHTQFPSSRSSLNPVQTIISRAAAEKLFGNMEGDCPSDWKTD	240

```

Query   361   STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG   420
Sbjct   241   STCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAASKG   300

Query   421   VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT   480
Sbjct   301   VGTALLLKLAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFT   360

Query   481   YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA   540
Sbjct   361   YINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNA   420

Query   541   AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK   600
Sbjct   421   AFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIK   480

Query   601   LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF   660
Sbjct   481   LTHDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDF   540

Query   661   GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK   720
Sbjct   541   GNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLK   600

Query   721   QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   760
Sbjct   601   QNNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   640

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3743

Number of extensions: 2118

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

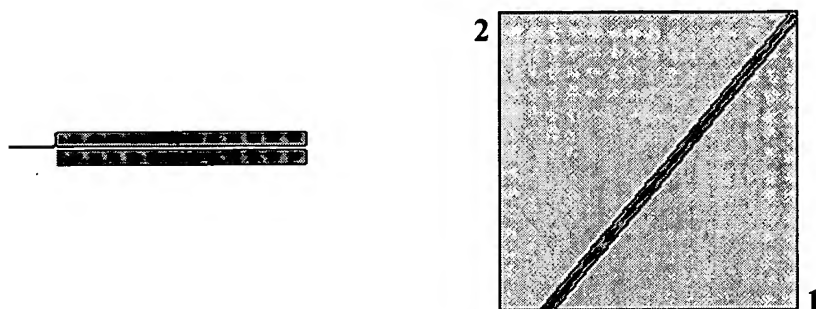
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
 Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314), Expect = 0.0

Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQUIDNO
 1 Query 122 LYWDDLKRKLSEKLDSTDTFTGTIKLLNENSYVPREAGSQKDNLALYVENQFREFKLSKV 181
 14 Sbjct 1 LYWDDLKRKLSEKLDSTDTFT TIKLLNENSYVPREAGSQKDNLALYVEN+FREFKLSKV 60
 Query 182 WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK 241
 Sbjct 61 WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK 120
 Query 242 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 301
 Sbjct 121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180
 Query 302 HLGTDGPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAELFGNMEGDCPSDWKTD 361
 Sbjct 181 HLGTDGPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAELFGNMEGDCPSDWKTD 240


```

Query   362   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct   241   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   300

Query   422   GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY   481
          GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY
Sbjct   301   GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY   360

Query   482   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct   361   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   420

Query   542   FPFLAYSGIPAVSFCFCEDTDYPYLGTMTDTYKELIERIPELNKVARAAAEVAGQFVIKL   601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTMTDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct   421   FPFLAYSGIPAVSFCFCEDTDYPYLGTMTDTYKELIERIPELNKVARAAAEVAGQFVIKL   480

Query   602   THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   661
          THDVELNLDYE  YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct   481   THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   540

Query   662   NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ   721
          NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ
Sbjct   541   NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ   600

Query   722   NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   760
          NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct   601   NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   639

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 3738
 Number of extensions: 2121
 Number of successful extensions: 1
 Number of sequences better than 10.0: 1
 Number of HSP's gapped: 1
 Number of HSP's successfully gapped: 1
 Length of query: 760
 Length of database: 1,433,654,390
 Length adjustment: 143
 Effective length of query: 617
 Effective length of database: 1,433,654,247
 Effective search space: 884564670399
 Effective search space used: 884564670399
 Neighboring words threshold: 9
 X1: 16 (7.3 bits)
 X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

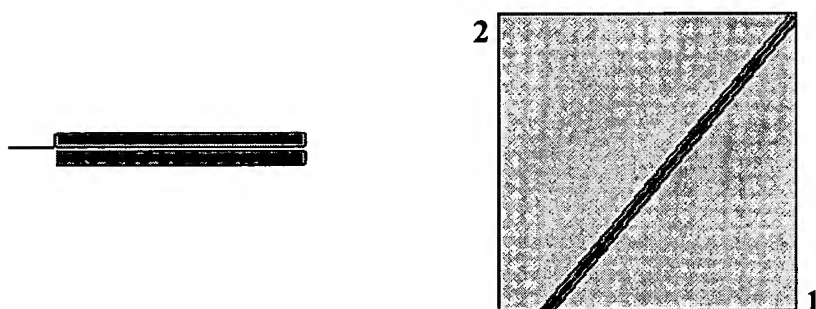
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
 Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314), Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQUENCE NO
 (15

Query	122	LYWDDLKRKLSEKLDSTDFGTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSKV	181
Sbjct	1	LYWDDLKRKLSEKLDSTDFT TIKLLNENSYPREAGSQKDENLALYVEN+ FREFKLSKV	60
Query	182	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK	241
Sbjct	61	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK	120
Query	242	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	301
Sbjct	121	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	180
Query	302	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	361
Sbjct	181	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	240

```

Query   362   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct   241   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   300

Query   422   GTALLLKLQAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY   481
          GTALLLKLQAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY
Sbjct   301   GTALLLKLQAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTY   360

Query   482   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct   361   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   420

Query   542   FPFLAYSGIPAVSFCFCEDTDYPYLGTMTDTYKELIERIPELNKVARAAAEVAGQFVIKL   601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTMTDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct   421   FPFLAYSGIPAVSFCFCEDTDYPYLGTMTDTYKELIERIPELNKVARAAAEVAGQFVIKL   480

Query   602   THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   661
          THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct   481   THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   540

Query   662   NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ   721
          NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ
Sbjct   541   NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ   600

Query   722   NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   760
          NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct   601   NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF   639

```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
0.318 0.135 0.399

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

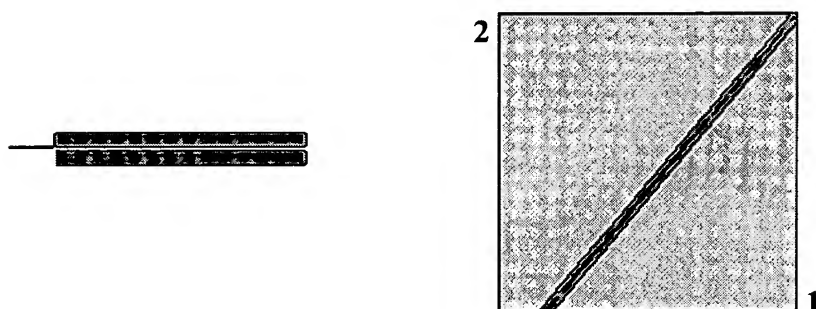
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
 Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: lc|seq_2
 Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314), Expect = 0.0
 Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

16
 Query 122 LYWDDLKRKLSEKLDSTDFGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV 181
 LYWDDLKRKLSEKLDSTDF TIKLLNENSYVPREAGSQKDENLALYVEN+ FREFKLSKV
 Sbjct 1 LYWDDLKRKLSEKLDSTDFSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV 60
 Query 182 WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK 241
 WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK
 Sbjct 61 WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK 120
 Query 242 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 301
 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA
 Sbjct 121 DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA 180
 Query 302 HLGTDGPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS 361
 HLGTDGPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS
 Sbjct 181 HLGTDGPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS 240

```

Query   362   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct   241   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   300

Query   422   GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSSLHLKAFTY   481
          GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSSLHLKAFTY
Sbjct   301   GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSSLHLKAFTY   360

Query   482   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct   361   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   420

Query   542   FPFLAYSGIPAVSFCFCEDTDYPYLGT'TMDTYKELIERIPELNKVARAAAEVAGQFVIKL   601
          FPFLAYSGIPAVSFCFCEDTDYPYLGT'TMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct   421   FPFLAYSGIPAVSFCFCEDTDYPYLGT'TMDTYKELIERIPELNKVARAAAEVAGQFVIKL   480

Query   602   THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   661
          THDVELNLDYE  YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct   481   THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   540

Query   662   NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ   721
          NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ
Sbjct   541   NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ   600

Query   722   NNGAFNETLFRNQLALATWT'IQGAANALSGDVWDIDNEF   760
          NNGAFNETLFRNQLALATWT'IQGAANALSGDVWDIDNEF
Sbjct   601   NNGAFNETLFRNQLALATWT'IQGAANALSGDVWDIDNEF   639

```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

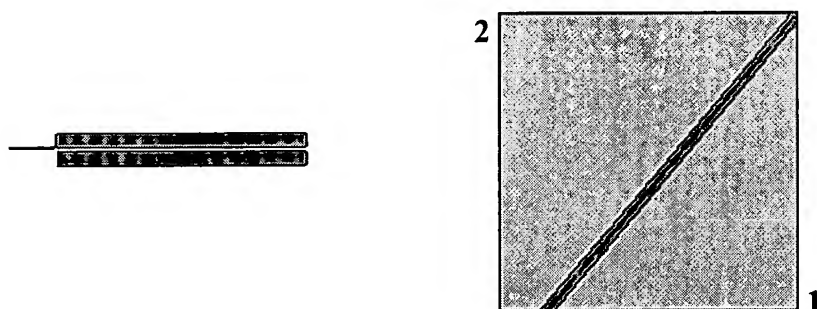
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

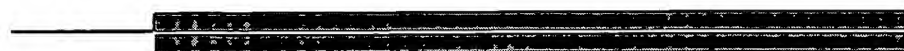
Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
 Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314), Expect = 0.0

Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQID NO

1	Query	122	LYWDDLKRKLSEKLDSTDFGTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSKV	181
			LYWDDLKRKLSEKLDSTDFT TIKLLNENSYPREAGSQKDENLALYVEN+FREFKLSKV	
17	Sbjct	1	LYWDDLKRKLSEKLDSTDFSTIKLLNENSYPREAGSQKDENLALYVENEFREFKLSKV	60
	Query	182	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK	241
			WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK	
	Sbjct	61	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKK	120
	Query	242	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	301
			DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	
	Sbjct	121	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	180
	Query	302	HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS	361
			HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS	
	Sbjct	181	HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS	240

```

Query 362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct 241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 300

Query 422 GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY 481
          GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY
Sbjct 301 GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY 360

Query 482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct 361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 420

Query 542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct 421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 480

Query 602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 661
          THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct 481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 540

Query 662 NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ 721
          NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ
Sbjct 541 NAEKTD RFVMKKLNDRVMRVEYHFLSPYVSPKESPF RHVFWGSGSHTLPALLENLKL RKQ 600

Query 722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 639

```

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

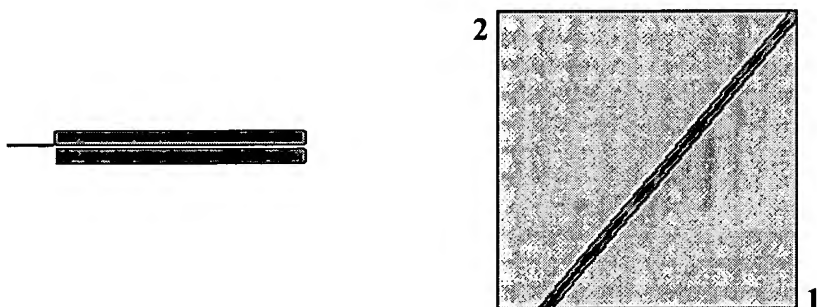
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]

Length = 760 (1 .. 760)

Sequence 2: lc|seq_2

Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314), Expect = 0.0

Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SeqIDNo

1	Query	122	LYWDDLKRKLSEKLDSTDFGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV	181
			LYWDDLKRKLSEKLDSTDFT TIKLLNENSYVPREAGSQKDENLALYVEN+FREFKLSKV	
18	Sbjct	1	LYWDDLKRKLSEKLDSTDFSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV	60
	Query	182	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLLENPGGYVAYSKAATVTGKLVHANFGTKK	241
			WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLLENPGGYVAYSKAATVTGKLVHANFGTKK	
	Sbjct	61	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLLENPGGYVAYSKAATVTGKLVHANFGTKK	120
	Query	242	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	301
			DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	
	Sbjct	121	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	180
	Query	302	HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAELFGNMEGDCPSDWKTDS	361
			HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAELFGNMEGDCPSDWKTDS	
	Sbjct	181	HLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAELFGNMEGDCPSDWKTDS	240

```

Query   362   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct   241   TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV   300

Query   422   GTALLLKLAQMFSMDVLKDGFPQRSRIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY   481
          GTALLLKLAQMFSMDVLKDGFPQRSRIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY
Sbjct   301   GTALLLKLAQMFSMDVLKDGFPQRSRIIFASWSAGDFGSGATEWLEGYLSSLHLKAFTY   360

Query   482   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct   361   INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA   420

Query   542   FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL   601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct   421   FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL   480

Query   602   THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   661
          THDVELNLDYE  YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct   481   THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG   540

Query   662   NAEKTDRLFVMKKLNDVRMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ   721
          NAEKTDRLFVMKKLNDVRMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ
Sbjct   541   NAEKTDRLFVMKKLNDVRMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ   600

Query   722   NNGAFNETLFRNQLALATWTIIQGAANALSGDVWDIDNEF   760
          NNGAFNETLFRNQLALATWTIIQGAANALSGDVWDIDNEF
Sbjct   601   NNGAFNETLFRNQLALATWTIIQGAANALSGDVWDIDNEF   639

```

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Sequences: 1
 Number of Hits to DB: 3738
 Number of extensions: 2121
 Number of successful extensions: 1
 Number of sequences better than 10.0: 1
 Number of HSP's gapped: 1
 Number of HSP's successfully gapped: 1
 Length of query: 760
 Length of database: 1,433,654,390
 Length adjustment: 143
 Effective length of query: 617
 Effective length of database: 1,433,654,247
 Effective search space: 884564670399
 Effective search space used: 884564670399
 Neighboring words threshold: 9
 X1: 16 (7.3 bits)
 X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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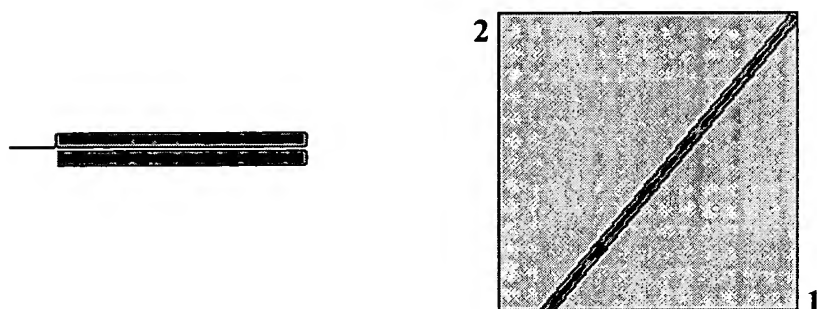
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
 Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: lcl|seq_2
 Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314), Expect = 0.0

Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQIDNO

1

19

Query	122	LYWDDLKRKLSEKLDSTDFGTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSKV	181
		LYWDDLKRKLSEKLDSTDF TIKLLNENSYPREAGSQKDENLALYVEN+ FREFKLSKV	
Sbjct	1	LYWDDLKRKLSEKLDSTDFSTIKLLNENSYPREAGSQKDENLALYVENEFREFKLSKV	60
Query	182	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK	241
		WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK	
Sbjct	61	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL V HANFGTKK	120
Query	242	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	301
		DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	
Sbjct	121	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	180
Query	302	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	361
		HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	
Sbjct	181	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	240

```

Query 362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct 241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 300

Query 422 GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSSLHLKAFTY 481
          GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSSLHLKAFTY
Sbjct 301 GTALLLKLAQMFSMDVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSSLHLKAFTY 360

Query 482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct 361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 420

Query 542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct 421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 480

Query 602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 661
          THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct 481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 540

Query 662 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ 721
          NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ
Sbjct 541 NAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRRHVFWGSGSHTLPALLENLKLKQ 600

Query 722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 639

```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
0.318 0.135 0.399

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

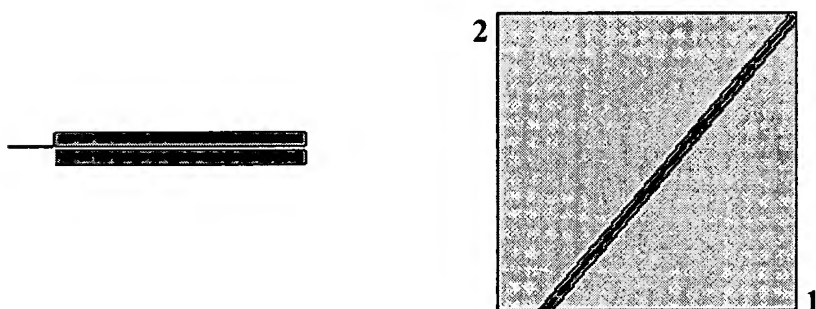
Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]

Length = 760 (1 .. 760)

Sequence 2: lc|seq_2

Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 1281 bits (3314), Expect = 0.0

Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQUIDNO

1	Query	122	LYWDDLKRKLSEKLDSTDFGTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKV	181
			LYWDDLKRKLSEKLDSTDF TIKLLNENSYVPREAGSQKDENLALYVEN+ FREFKLSKV	
20	Sbjct	1	LYWDDLKRKLSEKLDSTDFSTIKLLNENSYVPREAGSQKDENLALYVENEFREFKLSKV	60
	Query	182	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTKK	241
			WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTKK	
	Sbjct	61	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYS KAATVTGKLVHANFGTKK	120
	Query	242	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	301
			DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	
	Sbjct	121	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	180
	Query	302	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS	361
			HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS	
	Sbjct	181	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDS	240

```

Query 362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct 241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 300

Query 422 GTALLLKLAAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFTY 481
          GTALLLKLAAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFTY
Sbjct 301 GTALLLKLAAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGVATEWLEGYLSLHLKAFTY 360

Query 482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct 361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 420

Query 542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct 421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 480

Query 602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 661
          THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct 481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 540

Query 662 NAEKTD R FVMKKL NDRVMRVEYHFLSPYVSPKES PFRHVFWGSGSHTLPALLENLKLKQ 721
          NAEKTD R FVMKKL NDRVMRVEYHFLSPYVSPKES PFRHVFWGSGSHTLPALLENLKLKQ
Sbjct 541 NAEKTD R FVMKKL NDRVMRVEYHFLSPYVSPKES PFRHVFWGSGSHTLPALLENLKLKQ 600

Query 722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 639

```

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda K H
0.318 0.135 0.399

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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Taxonomy

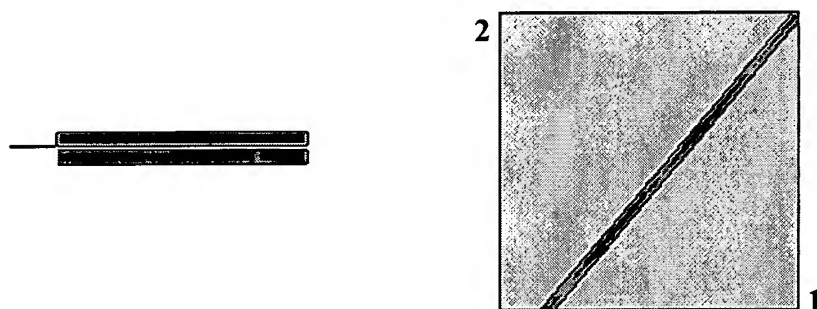
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
Masking character option X for protein, n for nucleotide Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
Length = 760 (1 .. 760)

Sequence 2: lc|seq_2
Length = 639 (1 .. 639)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1281 bits (3314), Expect = 0.0
Identities = 636/639 (99%), Positives = 637/639 (99%), Gaps = 0/639 (0%)

SEQUIDNO
1
21

Query	122	LYWDDLKRKLSEKLDSTDFGTIKLLNENSYPREAGSQKDENLALYVENQFREFKLSKV	181
		LYWDDLKRKLSEKLDSTDF TIKLLNENSYPREAGSQKDENLALYVEN+ FREFKLSKV	
Sbjct	1	LYWDDLKRKLSEKLDSTDFSTIKLLNENSYPREAGSQKDENLALYVENEFREFKLSKV	60
Query	182	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL VHANFGTKK	241
		WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL VHANFGTKK	
Sbjct	61	WRDQHFVKIQVKDSAQNSV IIVDKNGRLVYLVENPGGYVAYSKAATVTGKL VHANFGTKK	120
Query	242	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	301
		DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	
Sbjct	121	DFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHA	180
Query	302	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	361
		HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	
Sbjct	181	HLGTGDPYTPGFPSFNHTQFPSPRSSGLPNIPVQTISRAAA EKLFGNMEGDCPSDWKTDS	240

```

Query 362 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 421
          TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV
Sbjct 241 TCRMVTSESKNVKLTVSNVLKEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAGSGV 300

Query 422 GTALLLKLAAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFTY 481
          GTALLLKLAAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFTY
Sbjct 301 GTALLLKLAAQMFSDMVLKDGFPQRSIIIFASWSAGDFGSGATEWLEGYLSLHLKAFTY 360

Query 482 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 541
          INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA
Sbjct 361 INLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAA 420

Query 542 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 601
          FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL
Sbjct 421 FPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKL 480

Query 602 THDVELNLDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 661
          THDVELNLDYE YNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG
Sbjct 481 THDVELNLDYEEYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFG 540

Query 662 NAEKTDRFVMKKLNDVRMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLKQ 721
          NAEKTDRFVMKKLNDVRMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLKQ
Sbjct 541 NAEKTDRFVMKKLNDVRMRVEYHFLSPYVSPKESPFHRVFWGSGSHTLPALLENLKLKQ 600

Query 722 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 760
          NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF
Sbjct 601 NNGAFNETLFRNQLALATWTIQGAANALSGDVWDIDNEF 639

```

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
0.318 0.135 0.399

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 3738

Number of extensions: 2121

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



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OMIM

Taxonomy

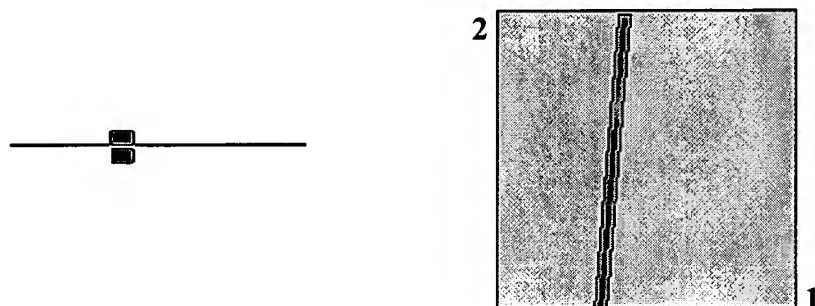
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
 Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|2144140|pir|S68317|transferrin receptor - guinea pig (fragment)
 >gi|1336700|gb|AAB35972.1| transferrin receptor; TfR [Cavia]
 Length = 63 (1 .. 63)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

Score = 118 bits (295), Expect = 2e-24
 Identities = 54/63 (85%), Positives = 57/63 (90%), Gaps = 0/63 (0%)

SEQIDNO

1 Query 261 KITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFHGHHLGTGDPYTPGFPSFNHTQ 320
 22 Sbjct 1 KITFAEKVANAESLNA+GVLIY+D TKFPI A+L FGH HLGTGDPYTPGFPSFNHTQ 60
 Query 321 FPP 323
 FPP
 Sbjct 61 FPP 63

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H

0.318 0.135 0.399

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 413

Number of extensions: 242

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 83 (36.6 bits)



Blast 2 Sequences results

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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

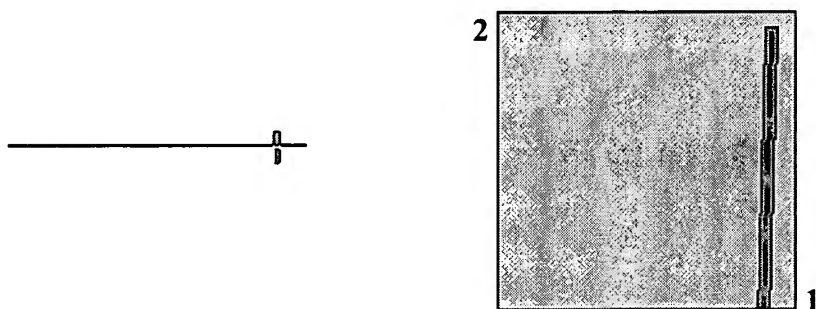
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]

Length = 760 (1 .. 760)

Sequence 2: gi|254113|gb|AAB22984.1|transferrin receptor [human, Peptide Partial, 17 aa]

Length = 17 (1 .. 17)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 40.4 bits (93), Expect = 0.60

Identities = 17/17 (100%), Positives = 17/17 (100%), Gaps = 0/17 (0%)

Query 680 RVEYHFLSPYVSPKESP 696
 RVEYHFLSPYVSPKESP
 23 Sbjct 1 RVEYHFLSPYVSPKESP 17

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 79
Number of extensions: 46
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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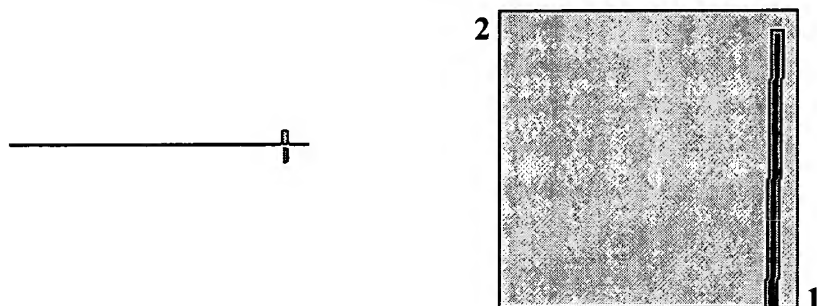
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☒ View option Standard
 Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation Align

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|957304|gb|AAB34741.1|transferrin receptor p95, TfR p95 {internal fragment} [human, prostatic-carcinoma cell line DU 145, Peptide Partial, 15 aa, segment 2 of 2]
 Length = 15 (1 .. 15)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 38.9 bits (89), Expect = 1.7

Identities = 15/15 (100%), Positives = 15/15 (100%), Gaps = 0/15 (0%)

SEQUENCE

1 Query 694 ESPFRHVFWSGSHT 708
 24 Sbjct 1 ESPFRHVFWSGSHT 15

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 74
Number of extensions: 45
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 760
Length of database: 1,433,654,390
Length adjustment: 143
Effective length of query: 617
Effective length of database: 1,433,654,247
Effective search space: 884564670399
Effective search space used: 884564670399
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 83 (36.6 bits)



Blast 2 Sequences results

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Taxonomy

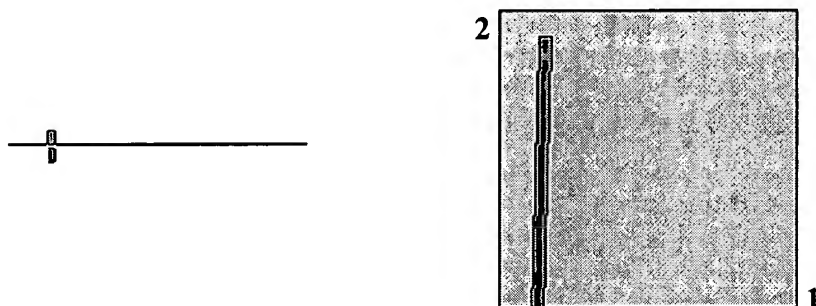
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☐ gap open: 11 gap extension: 1
 x_dropoff: 100 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
 Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|233761|gb|AAB19499.1|transferrin receptor [human, K562 erythroleukemia cells,
 Peptide Partial, 23 aa]
 Length = 23 (1 .. 23)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 37.7 bits (86), Expect = 3.9
 Identities = 18/22 (81%), Positives = 18/22 (81%), Gaps = 0/22 (0%)

SEQID NO
 1 Query 101 LAGTESPVREEPGEDFPAARRL 122
 LAG ESPV EEP EDFPAA RL
 25 Sbjct 1 LAGKESPVVEEPXEDFPAAXRL 22

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H

0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 108

Number of extensions: 69

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 143

Effective length of query: 617

Effective length of database: 1,433,654,247

Effective search space: 884564670399

Effective search space used: 884564670399

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 259 (99.8 bits)

X3: 259 (99.8 bits)

S1: 41 (21.7 bits)

S2: 83 (36.6 bits)



Blast 2 Sequences results

PubMed

Entrez

BLAST

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Taxonomy

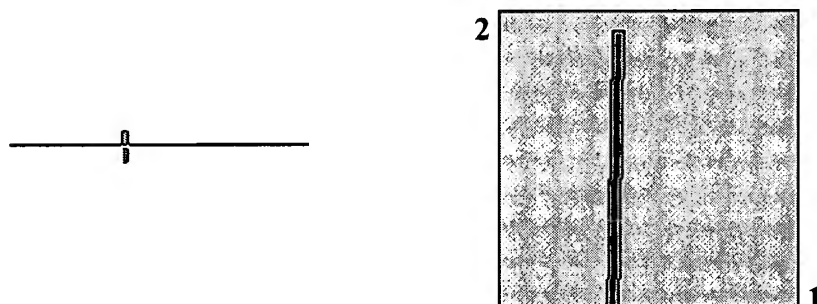
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.14 [May-07-2006]

Matrix BLOSUM62 ☐ gap open: 10 gap extension: 2
 x_dropoff: 200 expect: 10.000 wordsize: 3 Filter ☒ View option Standard ☐
 Masking character option X for protein, n for nucleotide ☐ Masking color option Black ☐
☐ Show CDS translation

Sequence 1: gi|14720550|ref|XP_052730.1|transferrin receptor (p90, CD71) [Homo sapiens]
 Length = 760 (1 .. 760)

Sequence 2: gi|957302|gb|AAB34739.1|transferrin receptor p95, TfR p95 {internal fragment} [human, prostatic-carcinoma cell line DU 145, Peptide Partial, 15 aa, segment 1 of 2]
 Length = 15 (1 .. 15)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 38.2 bits (82), Expect = 3.1
 Identities = 15/15 (100%), Positives = 15/15 (100%), Gaps = 0/15 (0%)

SEQIDNO

1 Query 288 FPIVNAELSFFGHAH 302
 FPIVNAELSFFGHAH
 26 Sbjct 1 FPIVNAELSFFGHAH 15

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.

Lambda K H
 0.318 0.135 0.399

Gapped
 Lambda K H

0.291 0.0750 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 10, Extension: 2

Number of Sequences: 1

Number of Hits to DB: 77

Number of extensions: 50

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 760

Length of database: 1,433,654,390

Length adjustment: 96

Effective length of query: 664

Effective length of database: 1,433,654,294

Effective search space: 951946451216

Effective search space used: 951946451216

Neighboring words threshold: 9

X1: 16 (7.3 bits)

X2: 476 (199.8 bits)

X3: 476 (199.8 bits)

S1: 41 (21.7 bits)

S2: 78 (36.5 bits)

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